Figure 24

(1)   Sequence of promoter CsVMV (Example 1A) (SEQ ID NO:1):

Tctagaaactagcttccagaaggtaattatccaagatgtagcatcaagaatccaatgtttacgggaaaaactatggaa

gtattatgtgagctcagcaagaagcagatcaatatgcggcacatatgcaacctatgttcaaaaatgaagaatgtacagatacaag

atcctatactgccagaatacgaagaagaatacgtagaaattgaaaaagaagaaccaggcgaagaaaagaatcttgaagacgta

agcactgacgacaacaatgaaaagaagaagataaggtcggtgattgtgaaagagacatagaggacacatgtaaggtggaaaa

tgtaagggcggaaagtaaccttatcacaaaggaatcttatcccccactacttatccttttatattttttccgtgtcattttttgcccttgagtt

ttcctatataaggaaccaagttcggcatttgtgaaaacaagaaaaaatttggtgtaagctattttctttgaagtactgaggatacaact

tcagagaaatttgtaagtttgta

     Total 531 bp

(2)   Sequence of zinc finger protein 2C7 binding site (Example 1A) (SEQ ID NO:2):
GCG TGG GCG GCG TGG GCG
     Total 18 bp.

(3)   Sequence of promoter pc7rbTATA (Example 1A) (SEQ ID NO:3):
Cccgggtatataataagcttggcattccggtactgttggtaaagccaccat
     Total 51 bp.

(4)   Sequence of pND3008 coding region (Example1B) (SEQ ID NO:4):

agcgtgacccggtcgtgcccctctctagagataatgagcattgcatgtctaagttataaaaaattaccacatattttttttg

tcacacttgtttgaagtgcagtttatctatctttatacatatatttaaactttactctacgaataatataatctatagtactacaataatatca

gtgttttagagaatcatatataaatgaacagttagacatggtctaaaggacaattgagtattttgacaacaggactctacagttttatcttt

ttagtgtgcatgtgttctcctttttttttttgcaaatagcttcacctatataatacttcatccattttattagtacatccatttagggtttaggg tt

aatggttttتatagactaatttttttagtacatctattttattctatttttagcctctaaattaagaaaactaaaactctatttttagtttttttattta

ataatttagatataaaatagaataaaataaagtgactaaaaattaaacaaatacccctttaagaaattaaaaaaactaaggaaacatttt

tcttgtttcgagtagataatgccagcctgttaaacgccgtcgacgagtctaacggacaccaaccagcgaaccagcagcgtcgcg

tcgggccaagcgaagcagacggcacggcatctctgtcgctgcctctggacccctctcgagagttccgctccaccgttggacttg

ctccgctgtcggcatccagaaattgcgtggcggagcggcagacgtgagccggcacggcaggcggcctcctcctcctctcacg

gcacggcagctacgggggattcctttcccaccgctccttcgctttcccttcctcgcccgccgtaataaatagacacccccctccaca

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Inventor: Carlos F. BARBAS, III et al.
Title: METHODS AND COMPOSITIONS TO MODULATE
EXPRESSION IN PLANTS

REPLACEMENT SHEET 25/42

ccctctttccccaacctcgtgttgttcggagcgcacacacacacaaccagatctcccccaaatccacccgtcggcacctccgctt

caaggtacgccgctcgtcctcccccccccccccctctctaccttctctagatcggcgttccggtccatggttagggcccggtagttc

tacttctgttcatgtttgtgttagatccgtgtttgtgttagatccgtgctgctagcgttcgtacacggatgcgacctgtacgtcagacac

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cttggttgtgatgatgtggtctggttgggcggtcgttctagatcggagtagaattctgtttcaaactacctggtggatttattaattttgg

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cgggttttactgatgcatatacagagatgcttttttgttcgcttggttgtgatgatgtggtgtggttgggcggtcgttcattcgttctagat

cggagtagaatactgtttcaaactacctggtgtatttattaattttggaactgtatgtgtgtgtcatacatcttcatagttacgagtttaag

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atatgctctaaccttgagtacctatctattataataaacaagtatgttttataattattttgatcttgatatacttggatgatggcatatgca

gcagctatatgtggatttttttagccctgccttcatacgctatttatttgcttggtactgtttctttttgtcgatgctcaccctgttgtttggtgt

tacttctgcaggtcgactctagaggatctatggcccaggcggccctcgagctccctatgcttgccctgtcgagtcctgcgatcgc

cgctttctaagtcggctgatctgaagcgccatatccgcatccacacaggccagaagcccttccagtgtcgaatatgcatgcgtaa

cttcagtcgtagtgaccaccttaccacccacatccgcacccacacaggcgagaagcctttgcctgtgacatttgtgggaggaag

tttgccaggagtgatgaacgcaagaggcataccaaaatccataccggtgagaagccctatgcttgccctgtcgagtcctgcgatc

gccgctttctaagtcggctgatctgaagcgccatatccgcatccacacaggccagaagcccttccagtgtcgaatatgcatgcgt

aacttcagtcgtagtgaccaccttaccacccacatccgcacccacacaggcgagaagcctttgcctgtgacatttgtgggagga

agtttgccaggagtgatgaacgcaagaggcataccaaaatccatttaagacagaaggactctagaactagtggccaggccggc

caggctagcccgaaaaagaaacgcaaagttgggcgcgccgacgcgctggacgatttcgatctcgacatgctgggttctgatgc

cctcgatgactttgacctggatatgttgggaagcgacgcattggatgactttgatctggacatgctcggctccgatgctctggacg

atttcgatctcgatatgttaattaactacccgtacgacgttccggactacgcttcttgagaattcgcggccgcgggccccgagcctag

ggaggagctcaagatcccccgaatttccccgatcgttcaaacatttggcaataaagtttcttaagattgaatcctgttgccggtcttg

cgatgattatcatctaatttctgttgaattacgttaagcatgtaataattaacatgtaatgcatgacgttatttatgagatgggttttttatga

ttagagtcccgcaattatacatttaatacgcgatagaaaacaaaatatagcgcgcaaactaggataaattatcgcgcgcggtgtca

tctatgttactagatccgggaattgggtac

Total:	3120 bp
ZmUbi promoter:	44 bp to 2026 bp
Six finger ZFP2C7:	2060 bp to 2588 bp
Nuclear localization signal:	2620 bp to 2641 bp
VP64 activation domain:	2641 bp to 2805 bp

HA eptitope tag: 2805 bp to 2836 bp

Nos terminator: 2884 bp to 3164 bp

(5)   Sequence of pND3018 coding region (Example 1B) (SEQ ID NO:5):

.agcgtgacccggtcgtgcccctctctagagataatgagcattgcatgtctaagttataaaaaattaccacatatttttttg

tcacacttgtttgaagtgcagtttatctatctttatacatatatttaaactttactctacgaataatataatctatagtactacaataatatca

gtgttttagagaatcatataaatgaacagttagacatggtctaaaggacaattgagtattttgacaacaggactctacagttttatctttt

ttagtgtgcatgtgttctcctttttttttgcaaatagcttcacctatataatacttcatccattttattagtacatccatttagggtttagggtt

aatggttttatagactaatttttttagtacatctatttattctattttagcctctaaattaagaaaactaaaactctattttagtttttttattta

ataatttagatataaaatagaataaaataaagtgactaaaaattaaacaaatacccttaagaaattaaaaaaactaaggaaacatttt

tcttgtttcgagtagataatgccagcctgttaaacgccgtcgacgagtctaacggacaccaaccagcgaaccagcagcgtcgcg

tcgggccaagcgaagcagacggcacggcatctctgtcgctgcctctggacccctctcgagagttccgctccaccgttggacttg

ctccgctgtcggcatccagaaattgcgtggcggagcggcagacgtgagccggcacggcaggcggcctcctcctcctctcacg

gcacggcagctacgggggattcctttcccaccgctccttcgctttcccttcctcgcccgccgtaataaatagacacccccctccaca

ccctctttccccaacctcgtgttgttcggagcgcacacacacacaaccagatctcccccaaatccacccgtcggcacctccgctt

caaggtacgccgctcgtcctccccccccccccctctctaccttctctagatcggcgttccggtccatggttagggcccggtagttc

tacttctgttcatgtttgtgttagatccgtgtttgtgttagatccgtgctgctagcgttcgtacacggatgcgacctgtacgtcagacac

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tttgtttcgttgcatagggtttggtttgcccttttcctttatttcaatatatgccgtgcacttgtttgtcgggtcatcttttcatgctttttttttgt

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cgggtttactgatgcatatacagagatgctttttgttcgcttggttgtgatgatgtggtgtggttgggcggtcgttcattcgttctagat

cggagtagaatactgtttcaaactacctggtgtatttattaattttggaactgtatgtgtgtgtcatacatcttcatagttacgagtttaag

atggatggaaatatcgatctaggataggtatacatgttgatgtgggttttactgatgcatatacatgatggcatatgcagcatctattc

atatgctctaaccttgagtacctatctattataataaacaagtatgttttataattattttgatcttgatatacttggatgatggcatatgca

gcagctatatgtggatttttttagccctgccttcatacgctatttatttgcttggtactgtttcttttgtcgatgctcaccctgttgtttggtgt

tacttctgcaggtcgactctagaggatccactagtgagccatgggctagcatggccgctgccgtgcgcatgaacatccagatgct

gctcgaagccgctgattatctggaacgccgggagcgcgaagccgagcacggctacgccagcatgctgccatatccgaaaaag

aaacgcaaggtggcccaggcggccctcgagctcccctatgcttgccctgtcgagtcctgcgatcgccgcttttctaagtcggctg

atctgaagcgccatatccgcatccacacaggccagaagcccttccagtgtcgaatatgcatgcgtaacttcagtcgtagtgacca

ccttaccacccacatccgcacccacacaggcgagaagccttttgcctgtgacatttgtgggaggaagtttgccaggagtgatgaa

cgcaagaggcataccaaaatccataccggtgagaagccctatgcttgccctgtcgagtcctgcgatcgccgcttttctaagtcgg

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gaacgcaagaggcataccaaaatccatttaagacagaaggactctagaactagtggccaggccggccagtacccgtacgacg

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acgttatttatgagatgggttttttatgattagagtcccgcaattatacatttaatacgcgatagaaaacaaaatatagcgcgcaaacta

ggataaaattatcgcgcgcggtgtcatctatgttactagatccgggaattccggaccggtaccagcggcc

Total:	3068 bp
ZmUbi promoter:	44 bp to 2026 bp
SID repression domain:	2066 bp to 2173 bp
Nuclear localization signal:	2174 bp to 2194 bp
Six finger ZFP2C7:	2207 bp to 2735 bp
HA eptitope tag:	2762 bp to 2791 bp
Nos terminator:	2820 bp to 3112 bp

(6)   Sequence of 6X2C7 binding site (SEQ ID NO:6):

Cgtgctagcgcgtgggcggcgtgggcgaacaagcgtgggcggcgtgggcgaacaagcgtgggcggcgtgggc

gactagtgctagcgcgtgggcggcgtgggcgaacaagcgtgggcggcgtgggcgaacaagcgtgggcggcgtgggcgac

tagtg

Total: 155 bp

(7)   Sequence of 3 finger protein C7 (SEQ ID NO:73):

Atggcccaggcggccctcgagccctatgcttgccctgtcgagtcctgcgatcgccgcttttctaagtcggctgatctg

aagcgccatatccgcatccacacaggccagaagcccttccagtgtcgaatatgcatgcgtaacttcagtcgtagtgaccacctta

ccacccacatccgcacccacacaggcgagaagccttttgcctgtgacatttgtgggaggaagtttgccaggagtgatgaacgca

agaggcataccaaaatccatttaagacagaaggactctagaactagtggccaggccggccaggctagc

Total: 314 bp

(8)   Amino acid sequence of 3 finger protein C7 (SEQ ID NO:74):

Maqaalepyacpvescdrrfsksadlkrhirihtgqkpfqcricmrnfsrsdhltthirthtgekpfacdicgrkfar

sderkrhtkihlrqkdsrtsgqagqas

Total: 105 aa

(9)   Sequence of zinc finger protein ZFPAp3 binding site (SEQ ID NO:7):

GAT GGA GTT GAA GAA GTA

Total: 18 bp

(10)   Sequence of zinc finger protein ZFPm1 and ZFPm2 binding site m12: (SEQ ID

NO:76):   GCC TCC TTC CTC CTC TCA CTC

Total: 21 bp

ZFPm1 binding site: compliment strand of 1 to 18

ZFPm2 binding site: compliment strand of 4 to 21

(11)   Sequence of zinc finger protein ZFPm3 and ZFPm4 binding site m34 (SEQ ID

NO:77):

GCC AAC TAC TAC GGC TCC CTC ACC

Total: 24 bp

ZFPm3 binding site: compliment strand of 1 to 18

ZFPm4 binding site: compliment strand of 7 to 24

(12)   Partial sequence of pMal-m1 (1-3300 bp) and zinc finger protein ZFPm1

        (2719-3270 bp) (SEQ ID NO:14):

ccgacaccatcgaatggtgcaaaacctttcgcggtatggcatgatagcgcccggaagagagtcaattcagggtggt

gaatgtgaaaccagtaacgttatacgatgtcgcagagtatgccggtgtctcttatcagaccgtttcccgcgtggtgaaccaggcca

gccacgtttctgcgaaaacgcgggaaaaagtggaagcggcgatggcggagctgaattacattcccaaccgcgtggcacaaca

actggcgggcaaacagtcgttgctgattggcgttgccacctccagtctggccctgcacgcgccgtcgcaaattgtcgcggcgat

taaatctcgcgccgatcaactgggtgccagcgtggtggtgtcgatggtagaacgaagcggcgtcgaagcctgtaaagcggcg

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caggccggccacctggccagccatcaacgcactcatactggcgagaagccatacaaatgtccagaatgtggcaagtctttctct

cggtctgacaatctcgtccggcaccaacgtactcacaccggtaaaaaaactagtggccaggccggccagtacccgtacgacgt

tccggactacgct

Total: 514 bp

Primer F1-f1 of ZFPm1: 2770 bp to 2850 bp

Primer F1-f2 of ZFPm1: 2740 bp to 2790 bp

Primer F2-f of ZFPm1: 2867 bp to 2940 bp

Primer F2-b of ZFPm1: 2824 bp to 2889 bp

Primer F3-b1 ZFPm1: 2916 bp to 2973 bp

Primer F3-b2 ZFPm1: 2953 bp to 3021 bp

Primer F4-f1 of ZFPm1: 3022 bp to 3102 bp

Primer F4-f2 of ZFPm1: 2992 bp to 3042 bp

Primer F5-f of ZFPm1: 3119 bp to 3192 bp

Primer F5-b of ZFPm1: 3076 bp to 3141 bp

Primer F6-b1 of ZFPm1: 3168 bp to 3225 bp

Primer F6-b2 of ZFPm1: 3205 bp to 3273 bp

(13)   Sequence of zinc finger protein ZFPm1

        (Translated from pMal-m1: 2719-3270 bp) (SEQ ID NO:75):

        Aqaalepgekpyacpecgksfsdpghlvrhqrthtgekpykcpecgksfsqrahlerhqrthtgekpykcpec

gksfsqssnlvrhqrthtgekpyacpecgksfsrsdnlvrhqrthtgekpykcpecgksfsrsdnlvrhqrthtgekpykcpe

cgksfsqaghlashqrthtgkktsgqag.

(14)   Partial sequence of pMal-m2 (1-3300 bp) and zinc finger protein ZFPm2

        (2719-3270 bp) (SEQ ID NO:15):

        ccgacaccatcgaatggtgcaaaacctttcgcggtatggcatgatagcgcccggaagagagtcaattcagggtggt

gaatgtgaaaccagtaacgttatacgatgtcgcagagtatgccggtgtctcttatcagaccgtttcccgcgtggtgaaccaggcca

gccacgtttctgcgaaaacgcgggaaaaagtggaagcggcgatggcggagctgaattacattcccaaccgcgtggcacaaca

actggcgggcaaacagtcgttgctgattggcgttgccacctccagtctggccctgcacgcgccgtcgcaaattgtcgcggcgat

taaatctcgcgccgatcaactgggtgccagcgtggtggtgtcgatggtagaacgaagcggcgtcgaagcctgtaaagcggcg

gtgcacaatcttctcgcgcaacgcgtcagtgggctgatcattaactatccgctggatgaccaggatgccattgctgtggaagctg

App No.: 09/765,555   Docket No.: 278012001420

Inventor: Carlos F. BARBAS, III et al.
Title: METHODS AND COMPOSITIONS TO MODULATE
EXPRESSION IN PLANTS

REPLACEMENT SHEET 31/42

cctgcactaatgttccggcgttatttcttgatgtctctgaccagacacccatcaacagtattattttctcccatgaagacggtacgcga

ctgggcgtggagcatctggtcgcattgggtcaccagcaaatcgcgctgttagcgggcccattaagttctgtctcggcgcgtctgc

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ggccaggcggtgaagggcaatcagctgttgcccgtctcactggtgaaaagaaaaaccaccctggcgcccaatacgcaaaccg

cctctccccgcgcgttggccgattcattaatgcagctggcacgacaggtttcccgactggaaagcgggcagtgagcgcaacgc

aattaatgtgagttagctcactcattaggcacaattctcatgtttgacagcttatcatcgactgcacggtgcaccaatgcttctggcgt

caggcagccatcggaagctgtggtatggctgtgcaggtcgtaaatcactgcataattcgtgtcgctcaaggcgcactcccgttct

ggataatgtttttgcgccgacatcataacggttctggcaaatattctgaaatgagctgttgacaattaatcatcggctcgtataatgt

gtggaattgtgagcggataacaatttcacacaggaaacagccagtccgtttaggtgttttcacgagcacttcaccaacaaggacc

atagattatgaaaactgaagaaggtaaactggtaatctggattaacggcgataaaggctataacggtctcgctgaagtcggtaag

aaattcgagaaagataccggaattaaagtcaccgttgagcatccggataaactggaagagaaattcccacaggttgcggcaact

ggcgatggccctgacattatcttctgggcacacgaccgctttggtggctacgctcaatctggcctgttggctgaaatcaccccgg

acaaagcgttccaggacaagctgtatccgtttacctgggatgccgtacgttacaacggcaagctgattgcttacccgatcgctgtt

gaagcgttatcgctgatttataacaaagatctgctgccgaacccgccaaaaacctgggaagagatcccggcgctggataaagaa

ctgaaagcgaaaggtaagagcgcgctgatgttcaacctgcaagaaccgtacttcacctggccgctgattgctgctgacggggggt

tatgcgttcaagtatgaaaacggcaagtacgacattaaagacgtgggcgtggataacgctggcgcgaaagcgggtctgaccttc

ctggttgacctgattaaaaacaaacacatgaatgcagacaccgattactccatcgcagaagctgcctttaataaaggcgaaacag

cgatgaccatcaacggcccgtgggcatggtccaacatcgacaccagcaaagtgaattatggtgtaacggtactgccgaccttca

agggtcaaccatccaaaccgttcgttggcgtgctgagcgcaggtattaacgccgccagtccgaacaaagagctggcaaaaga

gttcctcgaaaactatctgctgactgatgaaggtctggaagcggttaataaagacaaaccgctgggtgccgtagcgctgaagtct

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cggtctgacaatctcgtccggcaccaacgtactcacaccggtaaaaaaactagtggccaggccggccagtacccgtacgacgt

tccggactacgct

Total: 514 bp

Primer F1-f1 of ZFPm2: 2770 bp to 2850 bp

Primer F1-f2 of ZFP m2: 2740 bp to 2790 bp

Primer F2-f of ZFP m2: 2867 bp to 2940 bp

Primer F2-b of ZFPm2: 2824 bp to 2889 bp

Primer F3-b1 ZFPm2: 2916 bp to 2973 bp

Primer F3-b2 ZFPm2: 2953 bp to 3021 bp

Primer F4-f1 of ZFPm2: 3022 bp to 3102 bp

Primer F4-f2 of ZFPm2: 2992 bp to 3042 bp

Primer F5-f of ZFPm2: 3119 bp to 3192 bp

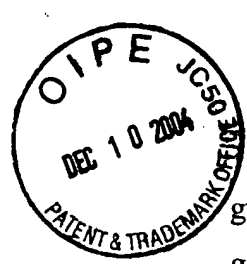Primer F5-b of ZFPm2: 3076 bp to 3141 bp

Primer F6-b1 of ZFPm2: 3168 bp to 3225 bp

Primer F6-b2 of ZFPm2: 3205 bp to 3273 bp

(15)   Partial sequence of pMal-m3 (1-3300 bp) and zinc finger protein ZFPm3
(2719-3270 bp) (SEQ ID NO:16):

ccgacaccatcgaatggtgcaaaacctttcgcggtatggcatgatagcgcccggaagagagtcaattcagggtggt

gaatgtgaaaccagtaacgttatacgatgtcgcagagtatgccggtgtctcttatcagaccgtttcccgcgtggtgaaccaggcca

gccacgtttctgcgaaaacgcgggaaaaagtggaagcggcgatggcggagctgaattacattcccaaccgcgtggcacaaca

actggcgggcaaacagtcgttgctgattggcgttgccacctccagtctggccctgcacgcgccgtcgcaaattgtcgcggcgat

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App No.: 09/765,555　　　　Docket No.: 278012001420
Inventor: Carlos F. BARBAS, III et al.
Title: METHODS AND COMPOSITIONS TO MODULATE
EXPRESSION IN PLANTS

REPLACEMENT SHEET 33/42

gttatatcccgccgttaaccaccatcaaacaggatttttcgcctgctggggcaaaccagcgtggaccgcttgctgcaactctctcag

ggccaggcggtgaagggcaatcagctgttgcccgtctcactggtgaaaagaaaaaccaccctggcgcccaatacgcaaaccg

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agtgactgccgcgaccttgctcgccatcaacgcactcatactggcgagaagccatacaaatgtccagaatgtggcaagtctttct

cccaatccagccatctcgtccggcaccaacgtactcacaccggtaaaaaaactagtggccaggccggccagtacccgtacgac

gttccggactacgct

Total:　514 bp

Primer F1-f1 of ZFPm3: 2770 bp to 2850 bp

App No.: 09/765,555   Docket No.: 278012001420
Inventor: Carlos F. BARBAS, III et al.
Title: METHODS AND COMPOSITIONS TO MODULATE
EXPRESSION IN PLANTS

REPLACEMENT SHEET 34/42

Primer F1-f2 of ZFP m3: 2740 bp to 2790 bp

Primer F2-f of ZFP m3: 2867 bp to 2940 bp

Primer F2-b of ZFPm3: 2824 bp to 2889 bp

Primer F3-b1 ZFPm3: 2916 bp to 2973 bp

Primer F3-b2 ZFPm3: 2953 bp to 3021 bp

Primer F4-f1 of ZFPm3: 3022 bp to 3102 bp

Primer F4-f2 of ZFPm3: 2992 bp to 3042 bp

Primer F5-f of ZFPm3: 3119 bp to 3192 bp

Primer F5-b of ZFPm3: 3076 bp to 3141 bp

Primer F6-b1 of ZFPm3: 3168 bp to 3225 bp

Primer F6-b2 of ZFPm3: 3205 bp to 3273 bp

(16)   <u>Partial sequence of pMal-m4 (1-3300 bp) and zinc finger protein ZFPm4</u>

        <u>(2719-3270 bp) (SEQ ID NO:17):</u>

ccgacaccatcgaatggtgcaaaacctttcgcggtatggcatgatagcgcccggaagagagtcaattcagggtggt

gaatgtgaaaccagtaacgttatacgatgtcgcagagtatgccggtgtctcttatcagaccgtttcccgcgtggtgaaccaggcca

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ccggactacgct

Total: 514 bp

Primer F1-f1 of ZFPm4: 2770 bp to 2850 bp

Primer F1-f2 of ZFPm4: 2740 bp to 2790 bp

Primer F2-f of ZFPm4: 2867 bp to 2940 bp

Primer F2-b of ZFPm4: 2824 bp to 2889 bp

Primer F3-b1 ZFPm4: 2916 bp to 2973 bp

Primer F3-b2 ZFPm4: 2953 bp to 3021 bp

Primer F4-f1 of ZFPm4: 3022 bp to 3102 bp

Primer F4-f2 of ZFPm4: 2992 bp to 3042 bp

Primer F5-f of ZFPm4: 3119 bp to 3192 bp

Primer F5-b of ZFPm4: 3076 bp to 3141 bp

Primer F6-b1 of ZFPm4: 3168 bp to 3225 bp

Primer F6-b2 of ZFPm4: 3205 bp to 3273 bp

(17)   Partial sequence of pMal-Ap3 (1-3300 bp) and zinc finger protein ZFPAp3
(2719-3270 bp) (SEQ ID NO:18):

ccgacaccatcgaatggtgcaaaacctttcgcggtatggcatgatagcgcccggaagagagtcaattcagggtggt

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aatgcgcgccattaccgagtccgggctgcgcgttggtgcggatatctcggtagtgggatacgacgataccgaagacagctcat

gttatatcccgccgttaaccaccatcaaacaggattttcgcctgctggggcaaaccagcgtggaccgcttgctgcaactctctcag

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cgttccggactacgct

Total: 514 bp

Primer F1-f1 of ZFPAp3: 2770 bp to 2850 bp

Primer F1-f2 of ZFPAp3: 2740 bp to 2790 bp

Primer F2-f of ZFPAp3: 2867 bp to 2940 bp

Primer F2-b of ZFPAp3: 2824 bp to 2889 bp

Primer F3-b1 ZFPAp3: 2916 bp to 2973 bp

Primer F3-b2 ZFPAp3: 2953 bp to 3021 bp

Primer F4-f1 of ZFPAp3: 3022 bp to 3102 bp

Primer F4-f2 of ZFPAp3: 2992 bp to 3042 bp

Primer F5-f of ZFPAp3: 3119 bp to 3192 bp

Primer F5-b of ZFPAp3: 3076 bp to 3141 bp

Primer F6-b1 of ZFPAp3: 3168 bp to 3225 bp

Primer F6-b2 of ZFPAp3: 3205 bp to 3273 bp

(18)   Sequence of oligo m12 (SEQ ID NO:19):

Biotin-GGa gcc tcc ttc ctc ctc tca ctc GGG TTTT CCC gag tga gag gag gaa gga ggc tCC

Total: 58 bp

Lower case sequence: ZFPm1 and ZFPm2 binding site m12

(19)   Sequence of oligo m34 (SEQ ID NO:20):

Biotin-GGa gcc aac tac tac ggc tcc ctc acc GGG TTTT CCC ggt gag gga gcc gta gta gtt ggc tCC

Total: 58 bp

Lower case sequence: ZFPm3 and ZFPm4 binding site m34

(20)   Sequence of oligo Ap3 (SEQ ID NO:21):

Biotin-GGt tac ttc ttc aac tcc atc GGG TTTT CCC gat gga gtt gaa gaa gta aCC

Total: 52 bp

Lower case sequence: ZFPAp3 binding site

(21)   Sequence of oligo NRI-1 (SEQ ID NO:22):

Biotin-GG ttc tac ccc tcc cac cgc GGG TTTT CCC gcg gtg gga ggg gta gaa CC

Total: 51 bp

(22)   Sequence of oligo NRI-2 (SEQ ID NO:23):

Biotin-GG tgc ggc gac tgc agc agc GGG TTTT CCC gct gct gca gtc gcc gca CC

Total: 51 bp

(23)   Sequence of oligo hHD-I (SEQ ID NO:24):

Biotin-GG ggc ccc gcc tcc gcc ggc GGG TTTT CCC gcc ggc gga ggc ggg gcc CC

Total: 51 bp

(24)   Sequence of oligo hHD-II (SEQ ID NO:25):

Biotin-GG ggc agc ccc cac ggc gcc GGG TTTT CCC ggc gcc gtg ggg gct gcc CC

Total: 51 bp

(25)   Sequence of oligo c5p1-g (SEQ ID NO:26):

Biotin-GG gac acc ccc aac ccc gcc GGG TTTT CCC ggc ggg gtt ggg ggt gtc CC

Total: 51 bp

(26)   Sequence of oligo c5p3-g (SEQ ID NO:27):

Biotin-GG ctc tgc tca tcc cac tac GGG TTTT CCC gta gtg gga tga gca gag CC

Total: 51 bp

(27)   Sequence of oligo B3c2 (SEQ ID NO:28):

Biotin-GG acc cac cgc gtc ccc tcc GGG TTTT CCC gga ggg gac gcg gtg ggt CC

Total: 51 bp

(28)   Sequence of oligo e2c-g (SEQ ID NO:29):

Biotin-GG cac tgc ggc tcc ggc ccc GGG TTTT CCC ggg gcc gga gcc gca gtg CC

Total: 51 bp

(29)   Sequence of primer Ap3-F (SEQ ID NO:30):

GGCGAGAGGGAAGATCCAG

Total: 19 bp

(30)   Sequence of primer NZlib5' (SEQ ID NO:31):

GGCCCAGGCGGCCCTCGAGC

Total: 20 bp

(31)   Sequence of primer Ap3f4-R (SEQ ID NO:32):

CTCCTCTAATACGACTCACTATAGGGACACTCACCTAGCCTCTG

Total: 44 bp

(32)   Sequence of primer m4f3-R (SEQ ID NO:33):

CCTCGCAAGATCACGACAATC

Total: 21 bp

(33)   Sequence of quantitative PCR probe for AP3 (SEQ ID NO:34):

CCATTTCATCCTCAAGACGACGCAGCT

Total: 27 bp

(34)   Sequence of quantitative PCR primer for AP3 (Forward) (SEQ ID NO:35):

TTTGGACGAGCTTGACATTCAG

Total: 22 bp

(35)   Sequence of quantitative PCR primer for AP3 (Reverse) (SEQ ID NO:36):

CGCGAACGAGTTTGAAAGTG

Total: 20 bp

(36)   Sequence of 2C7-SID (Figure 3) (SEQ ID NO:66):

gacggatcgggagatctcccgatcccctatggtcgactctcagtacaatctgctctgatgccgcatagttaagccagta
tctgctccctgcttgtgtgttggaggtcgctgagtagtgcgcgagcaaaatttaagctacaacaaggcaaggcttgaccgacaatt
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REPLACEMENT SHEET 41/42

ccacccacatccgcacccacacaggcgagaagcctttttgcctgtgacatttgtgggaggaagtttgccaggagtgatgaacgca
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gtgctcatcattggaaaacgttcttcggggcgaaaactctcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgt
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